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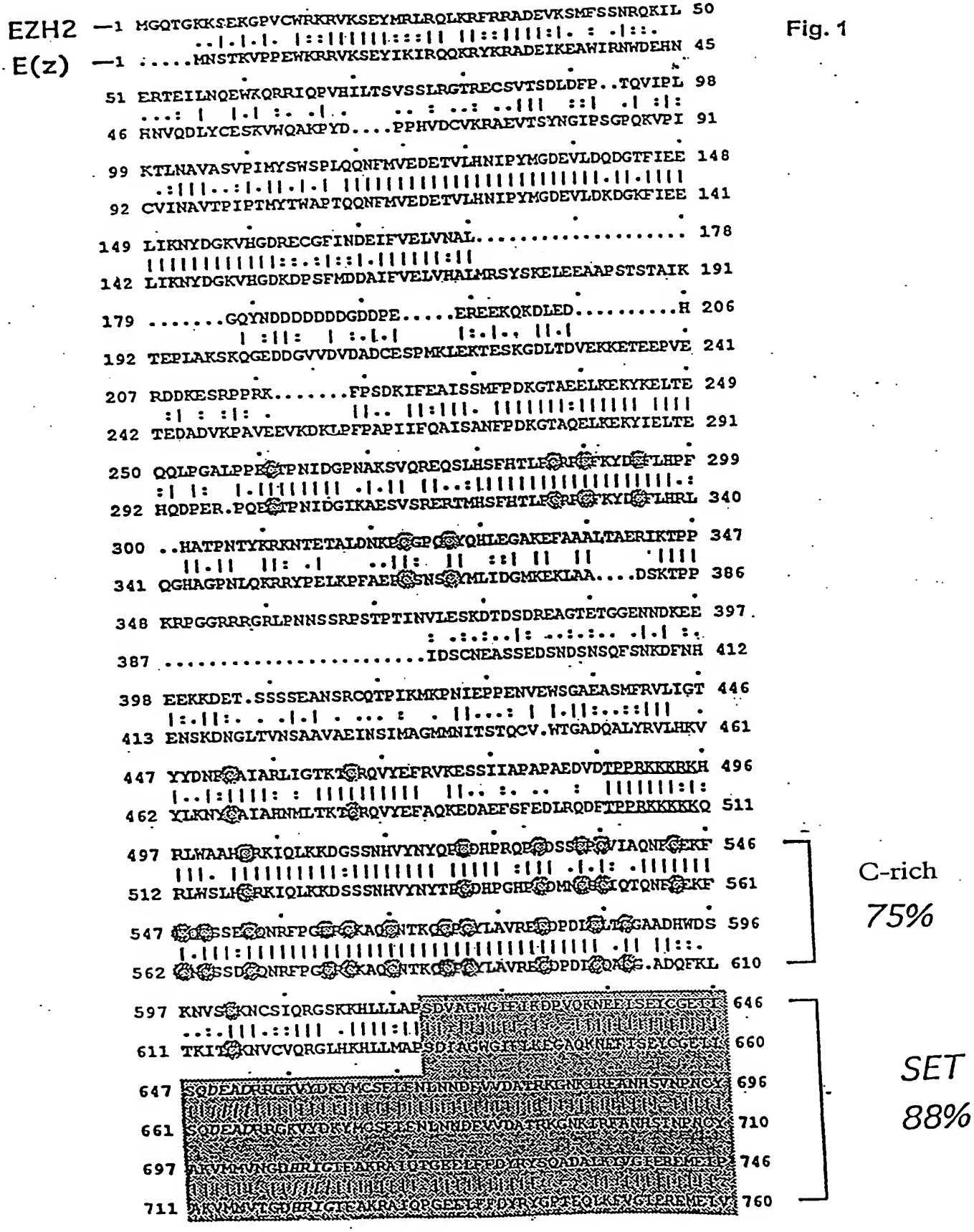
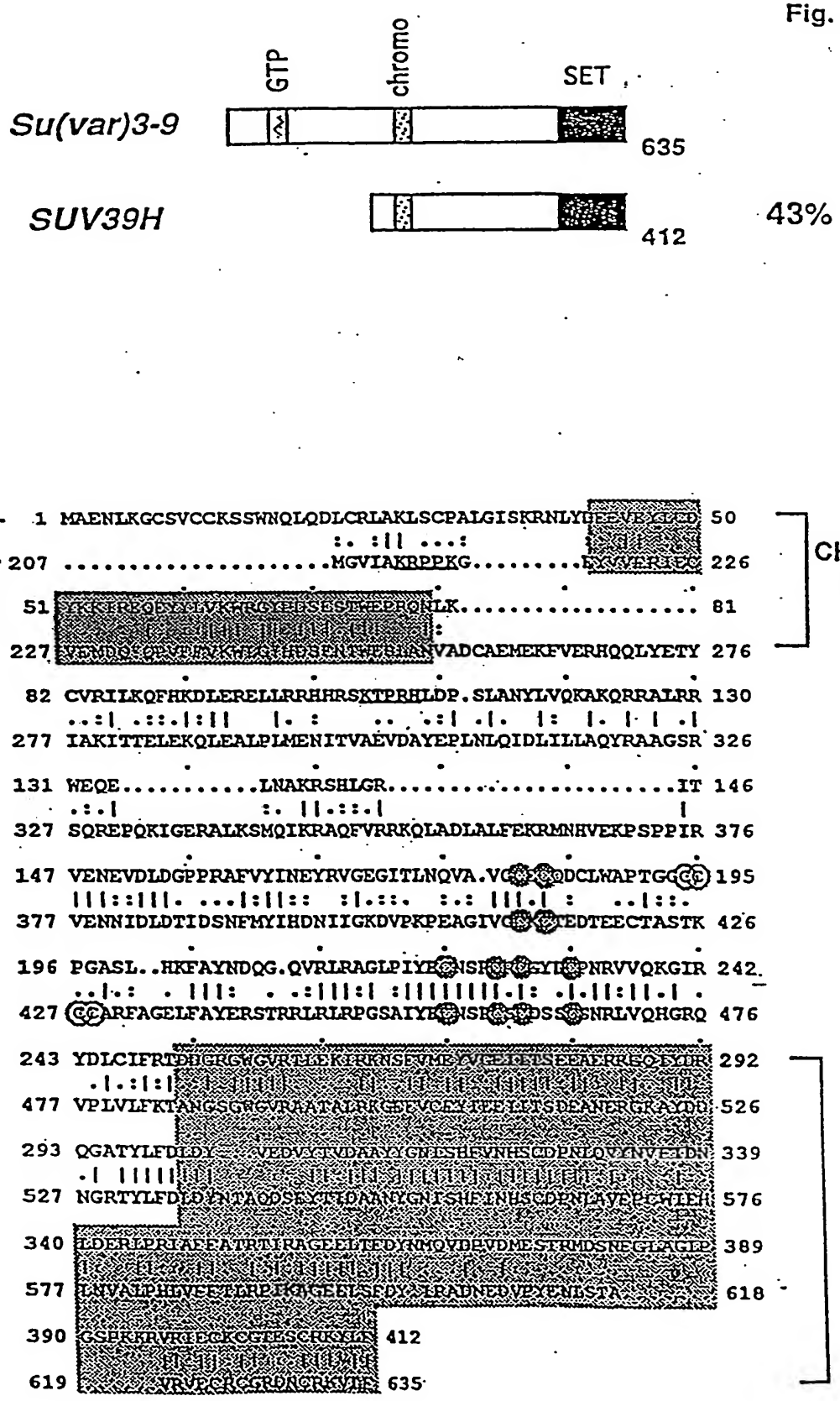


Fig. 1

Fig. 2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chromo
SET
Su(var)3-9
635
SUV39H
412
43%
Su(var)3-9
SUV39H
CHROMO
39 %
SET
51 %

ABERRANT TRANSCRIPTS

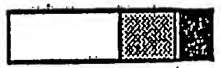
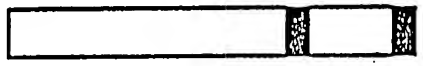
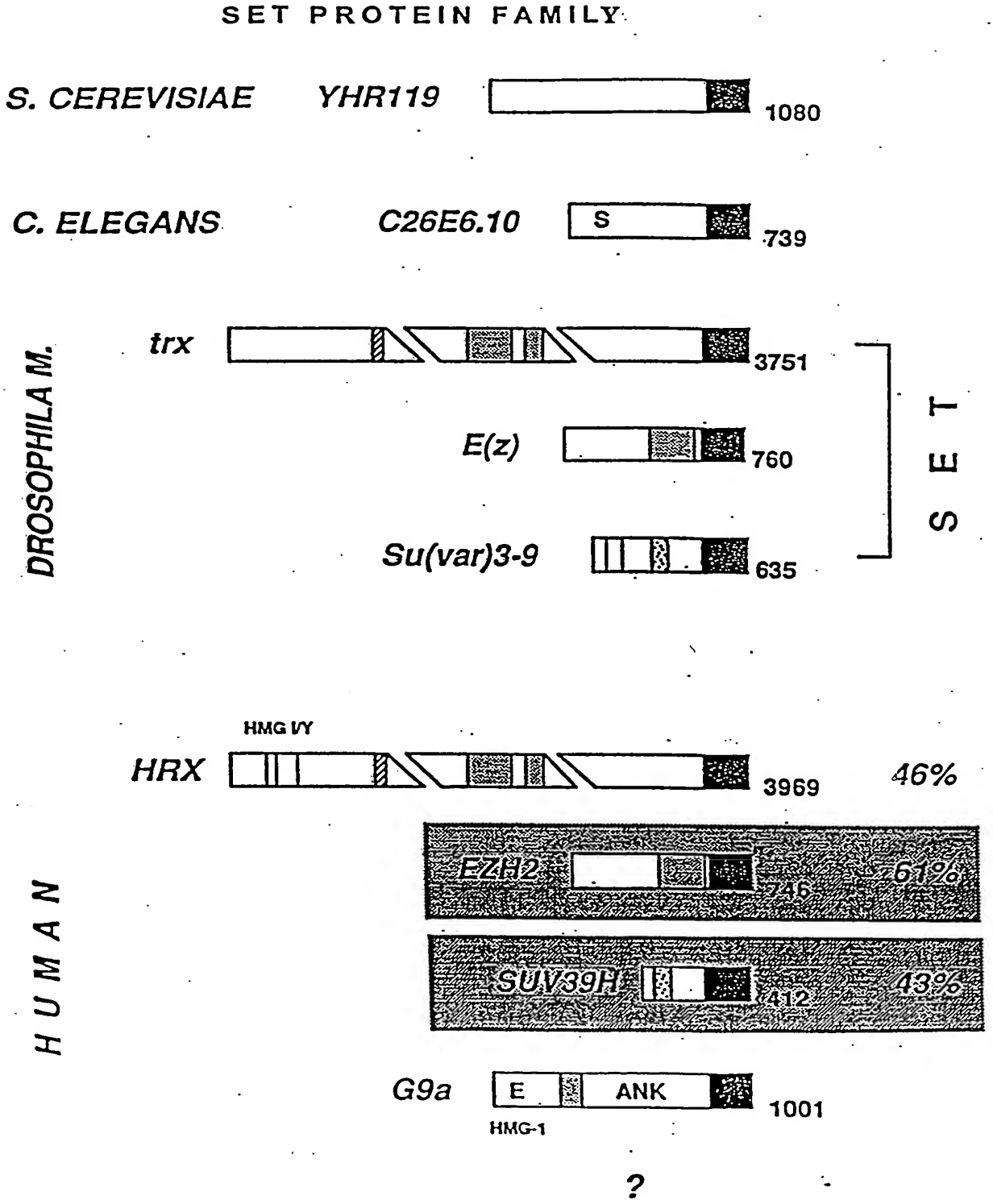
11q23	TRANSLOCATIONS LEUKAEMIA		*ALL-1*	*HRX*
17q21	UNSTABLE REGION BREAST CANCER (BRCA1)		*B52*	*EZH1*
Xp11	TRANSLOCATIONS SYNOVIAL SARCOMA (OATL1)		*MG-44*	*SUV39H*
6p21	*(MHC III)* AUTOIMMUNE DISEASES	*?*		*G9a*
?	MYELOID TUMOURS		*KG-1*	*?*

Fig. 3

Fig. 4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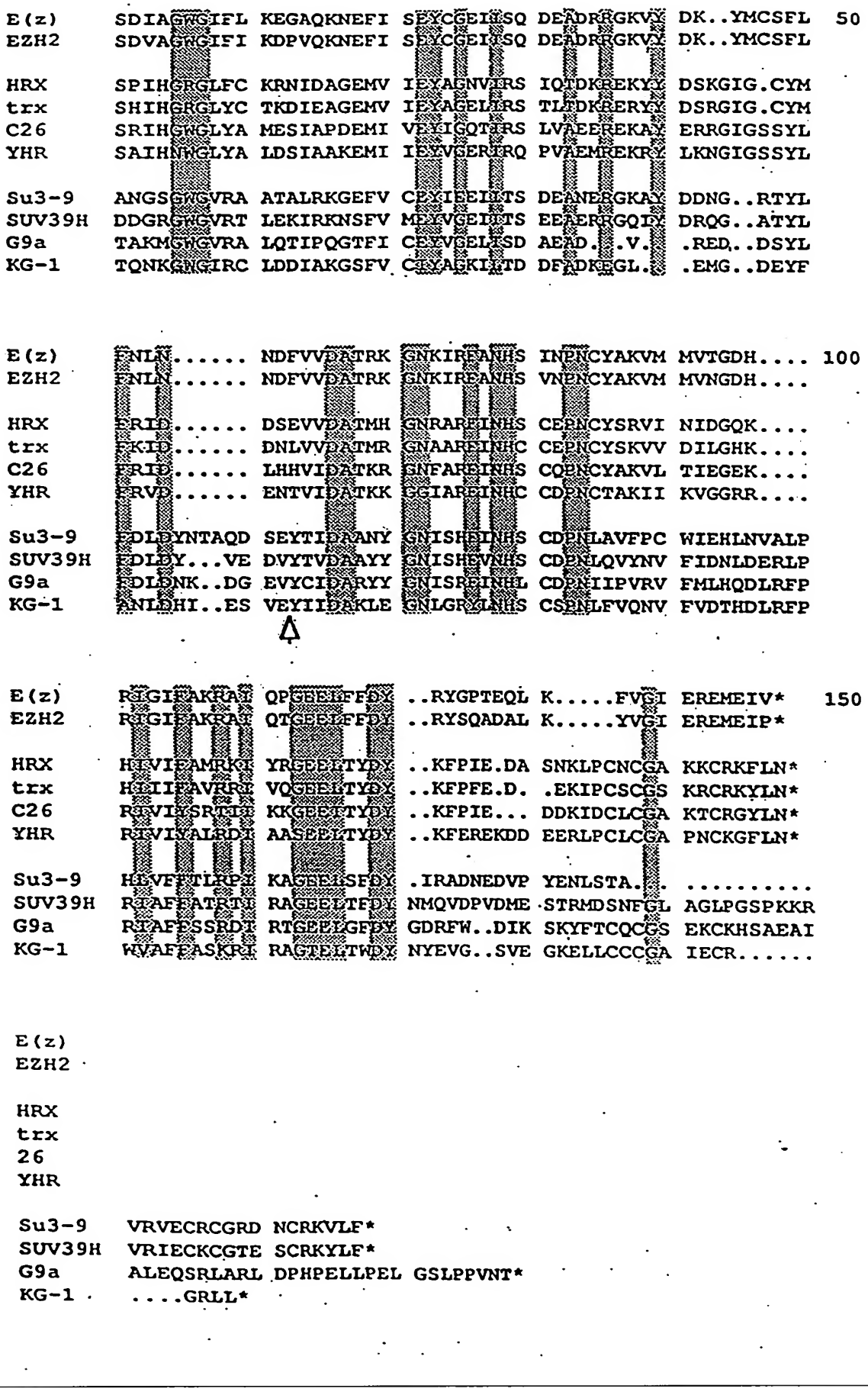
YHR119
1080
C. ELEGANS
C26E6.10
S
739
DROSOPHILA M.
trx
3751
E(z)
760
Su(var)3-9
635
SET
HUMAN
HMG I/Y
HRX
3969
46%
EZH2
746
61%
SUV39H
412
43%
G9a
E
ANK
1001
HMG-1
?

Fig. 5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HRX SPIHGRGLFC KRNIDAGEMV IEYAGNVIRS IQTDKREKYY DSKGIG.CYM
trx SHIHGRGLYC TKDIEAGEMV IEYAGELIRS TLTDKRERYY DSRGIG.CYM
C26 SRIHGWGLYA MESIAPDEMI VEYIGQTIRS LVAEEREKAY ERRGIGSSYL
YHR SAIHNWGLYA LDSIAAKEMI IEYVGERIRQ PVAEMREKRY LKNGIGSSYL
Su3-9 ANGSGWGVRA ATALRKGEFV CEYIEEIITS DEANERGKAY DDNG..RTYL
SUV39H DDGRGWGVRT LEKIRKNSFV MEYVGEIITS EEAERRGQIY DRQG..ATYL
G9a TAKMGWGVRA LQTIPQGTFI CEYVGELISD AEAD...V.. .RED..DSYL
KG-1 TQNKGNGIRC LDDIAKGSFV CEYAGKIITD DFADKEGL.. .EMG..DEYF
E(z) FNLN..... NDFVVDATRK GNKIRFANHS INPNCYAKVM MVTGDH.... 100
EZH2 FNLN..... NDFVVDATRK GNKIREANHS VNPNCYAKVM MVNGDH....
HRX FRID..... DSEVVDATMH GNRARFINHS CEPNCYSRVI NIDGQK....
trx FKID..... DNLVVDATMR GNAARFINHC CEPNCYSKVV DILGHK....
C26 FRID..... LHHVIDATKR GNFAREINHS CQPNCYAKVL TIEGEK....
YHR FRVD..... ENTVIDATKK GGIAREINHC CDPNCTAKII KVGGRR....
Su3-9 FDLDYNTAQD SEYTIDAANY GNISHFINHS CDPNLAVFPC WIEHLNVALP
SUV39H FDLDY...VE DVYTVDAAYY GNISHFVNHS CDPNLQVYNV FIDNLDERLP
G9a FDLDNK..DG EVYCIDARYY GNISRFINHL CDPNIIPVRV FMLHQDLRFP
KG-1 ANLDHI..ES VEYIIDAKLE GNLGRYLNHS CSPNLFVQNV FVDTHDLRFP
E(z) RIGIFAKRAI QPGEELFFDY ..RYGPTEQL K.....FVGI EREMEIV* 150
EZH2 RIGIFAKRAI QTGEELFFDY ..RYSQADAL K.....YVGI EREMEIP*
HRX HIVIFAMRKI YRGEELTYDY ..KFPIE.DA SNKLPCNCGA KKCRKFLN*
trx HLIIFAVRRI VQGEELTYDY ..KFPFE.D. .EKIPCSCGS KRCRKYLN*
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Su3-9 HLVFFTLRPI KAGEELSFDY .IRADNEDVP YENLSTA... .....
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E(z)
EZH2
HRX
trx
26
YHR
Su3-9 VRVECRCGRD NCRKVLF*
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KG-1 ....GRLL*

Fig. 6/1

EZH2 length: 2600bp (coding: 90 - 2330)

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  61  CGAGTCGGCGCGCGGGACGAAGAATAATCATGGGCCAGACTGGGAAGAAATCTGAGAAGG  120
                                  M  G  Q  T  G  K  K  S  E  K  G
 121  GACCAGTTTGTTGGCGGAAGCGTGTAAAATCAGAGTACATGCGACTGAGACAGCTCAAGA  180
        P  V  C  W  R  K  R  V  K  S  E  Y  M  R  L  R  Q  L  K  R
 181  GGTTCAGACGAGCTGATGAAGTAAAGAGTATGTTTAGTTCCAATCGTCAGAAAATTTTGG  240
        F  R  R  A  D  E  V  K  S  M  F  S  S  N  R  Q  K  I  L  E
 241  AAAGAACGGAAATCTTAAACCAAGAATGGAAACAGCGAAGGATACAGCCTGTGCACATCC  300
        R  T  E  I  L  N  Q  E  W  K  Q  R  R  I  Q  P  V  H  I  L
 301  TGACTTCTGTGAGCTCATTGCGCGGGACTAGGGAGTGTTCGGTGACCAGTGACTTGGATT  360
        T  S  V  S  S  L  R  G  T  R  E  C  S  V  T  S  D  L  D  F
 361  TTCCAACACAAGTCATCCCATTAAAGACTCTGAATGCAGTTGCTTCAGTACCCATAATGT  420
        P  T  Q  V  I  P  L  K  T  L  N  A  V  A  S  V  P  I  M  Y
 421  ATTCTTGGTCTCCCCTACAGCAGAATTTTATGGTGGAAGATGAAACTGTTTTACATAACA  480
        S  W  S  P  L  Q  Q  N  F  M  V  E  D  E  T  V  L  H  N  I
 481  TTCCTTATATGGGAGATGAAGTTTTAGATCAGGATGGTACTTTCATTGAAGAACTAATAA  540
        P  Y  M  G  D  E  V  L  D  Q  D  G  T  F  I  E  E  L  I  K
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        N  Y  D  G  K  V  H  G  D  R  E  C  G  F  I  N  D  E  I  F
 601  TTGTGGAGTTGGTGAATGCCCTTGGTCAATATAATGATGATGACGATGATGATGATGGAG  660
        V  E  L  V  N  A  L  G  Q  Y  N  D  D  D  D  D  D  D  G  D
 661  ACGATCCTGAAGAAAGAGAAGAAAAGCAGAAAGATCTGGAGGATCACCGAGATGATAAAG  720
        D  P  E  E  R  E  E  K  Q  K  D  L  E  D  H  R  D  D  K  E
 721  AAAGCCGCCCACCTCGGAAATTTCCTTCTGATAAAATTTTTGAAGCCATTTCCTCAATGT  780
        S  R  P  P  R  K  F  P  S  D  K  I  F  E  A  I  S  S  M  F
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        V  Q  R  E  Q  S  L  H  S  F  H  T  L  F  C  R  R  C  F  K
 961  AATATGACTGCTTCCTACATCCTTTTCATGCAACACCCAACACTTATAAGCGGAAGAACA 1020
        Y  D  C  F  L  H  P  F  H  A  T  P  N  T  Y  K  R  K  N  T
1021  CAGAAACAGCTCTAGACAACAAACCTTGTGGACCACAGTGTTACCAGCATTTGGAGGGAG 1080
        E  T  A  L  D  N  K  P  C  G  P  Q  C  Y  Q  H  L  E  G  A
1081  CAAAGGAGTTTGCTGCTGCTCTCACCGCTGAGCGGATAAAGACCCCACCAAAACGTCCAG 1140
        K  E  F  A  A  A  L  T  A  E  R  I  K  T  P  P  K  R  P  G
```

Fig. 6/2

```
1141  GAGGCCGCAGAAGAGGACGGCTTCCCAATAACAGTAGCAGGCCCAGCACCCCCACCATTA  1200
        G  R  R  R  G  R  L  P  N  N  S  S  R  P  S  T  P  T  I  N

1201  ATGTGCTGGAATCAAAGGATACAGACAGTGATAGGGAAGCAGGGACTGAAACGGGGGGAG  1260
        V  L  E  S  K  D  T  D  S  D  R  E  A  G  T  E  T  G  G  E

1261  AGAACAATGATAAAGAAGAAGAAGAGAAGAAAGATGAAACTTCGAGCTCCTCTGAAGCAA  1320
        N  N  D  K  E  E  E  E  K  K  D  E  T  S  S  S  S  E  A  N

1321  ATTCTCGGTGTCAAACACCAATAAAGATGAAGCCAAATATTGAACCTCCTGAGAATGTGG  1380
        S  R  C  Q  T  P  I  K  M  K  P  N  I  E  P  P  E  N  V  E

1381  AGTGGAGTGGTGCTGAAGCCTCAATGTTTAGAGTCCTCATTGGCACTTACTATGACAATT  1440
        W  S  G  A  E  A  S  M  F  R  V  L  I  G  T  Y  Y  D  N  F

1441  TCTGTGCCATTGCTAGGTTAATTGGGACCAAAACATGTAGACAGGTGTATGAGTTTAGAG  1500
        C  A  I  A  R  L  I  G  T  K  T  C  R  Q  V  Y  E  F  R  V

1501  TCAAAGAATCTAGCATCATAGCTCCAGCTCCCGCTGAGGATGTGGATACTCCTCCAAGGA  1560
        K  E  S  S  I  I  A  P  A  P  A  E  D  V  D  T  P  P  R  K

1561  AAAAGAAGAGGAAACACCGGTTGTGGGCTGCACACTGCAGAAAGATACAGCTGAAAAAGG  1620
        K  K  R  K  H  R  L  W  A  A  H  C  R  K  I  Q  L  K  K  D

1621  ACGGCTCCTCTAACCATGTTTACAACTATCAACCCTGTGATCATCCACGGCAGCCTTGTG  1680
        G  S  S  N  H  V  Y  N  Y  Q  P  C  D  H  P  R  Q  P  C  D

1681  ACAGTTCGTGCCCTTGTGTGATAGCACAAAATTTTTGTGAAAAGTTTTGTCAATGTAGTT  1740
        S  S  C  P  C  V  I  A  Q  N  F  C  E  K  F  C  Q  C  S  S

1741  CAGAGTGTCAAAACCGCTTTCCGGGATGCCGCTGCAAAGCACAGTGCAACACCAAGCAGT  1800
        E  C  Q  N  R  F  P  G  C  R  C  K  A  Q  C  N  T  K  Q  C

1801  GCCCGTGCTACCTGGCTGTCCGAGAGTGTGACCCTGACCTCTGTCTTACTTGTGGAGCCG  1860
        P  C  Y  L  A  V  R  E  C  D  P  D  L  C  L  T  C  G  A  A

1861  CTGACCATTGGGACAGTAAAAATGTGTCCTGCAAGAACTGCAGTATTCAGCGGGGCTGCA  1920
        D  H  W  D  S  K  N  V  S  C  K  N  C  S  I  Q  R  G  S  K

1921  AAAAGCATCTATTGCTGGCACCATCTGACGTGGCAGGCTGGGGGATTTTTATCAAAGATC  1980
        K  H  L  L  L  A  P  S  D  V  A  G  W  G  I  F  I  K  D  P

1981  CTGTGCAGAAAAATGAATTCATCTCAGAATACTGTGGAGAGATTATTTCTCAAGATGAAG  2040
        V  Q  K  N  E  F  I  S  E  Y  C  G  E  I  I  S  Q  D  E  A

2041  CTGACAGAAGAGGGAAAGTGTATGATAAATACATGTGCAGCTTTCTGTTCAACTTGAACA  2100
        D  R  R  G  K  V  Y  D  K  Y  M  C  S  F  L  F  N  L  N  N

2101  ATGATTTTGTGGTGGATGCAACCCGCAAGGGTAACAAAATTCGTTTTGCAAATCATTCGG  2160
        D  F  V  V  D  A  T  R  K  G  N  K  I  R  F  A  N  H  S  V

2161  TAAATCCAAACTGCTATGCAAAAGTTATGATGGTTAACGGTGATCACAGGATAGGTATTT  2220
        N  P  N  C  Y  A  K  V  M  M  V  N  G  D  H  R  I  G  I  F

2221  TTGCCAAGAGAGCCATCCAGACTGGCGAAGAGCTGTTTTTTGATTACAGATACAGCCAGG  2280
        A  K  R  A  I  Q  T  G  E  E  L  F  F  D  Y  R  Y  S  Q  A
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Fig. 6/3

```
2281  CTGATGCCCTGAAGTATGTCGGCATCGAAAGAGAAATGGAAATCCCTTGACATCTGCTAC  2340
        D  A  L  K  Y  V  G  I  E  R  E  M  E  I  P  *
2341  CTCCTCCCCCTCCTCTGAAACAGCTGCCTTAGCTTCAGGAACCTCGAGTACTGTGGGCAA  2400
2401  TTTAGAAAAAGAACATGCAGTTTGAAATTCTGAATTTGCAAAGTACTGTAAGAATAATTT  2460
2461  ATAGTAATGAGTTTAAAAATCAACTTTTTATTGCCTTCTCACCAGCTGCAAAGTGTTTTG  2520
2521  TACCAGTGAATTTTTGCAATAATGCAGTATGGTACATTTTTCAACTTTGAATAAAGAATA  2580
2581  CTTGAACTTGTCAAAAAAAA  2600
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Fig. 7/1

SUV39H length: 2732 bp (coding: 45 - 1284)

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        G  C  S  V  C  C  K  S  S  W  N  Q  L  Q  D  L  C  R  L  A

 121  CCAAGCTCTCCTGCCCTGCCCTCGGTATCTCTAAGAGGAACCTCTATGACTTTGAAGTCG  180
        K  L  S  C  P  A  L  G  I  S  K  R  N  L  Y  D  F  E  V  E

 181  AGTACCTGTGCGATTACAAGAAGATCCGCGAACAGGAATATTACCTGGTGAAATGGCGTG  240
        Y  L  C  D  Y  K  K  I  R  E  Q  E  Y  Y  L  V  K  W  R  G

 241  GATATCCAGACTCAGAGAGCACCTGGGAGCCACGGCAGAATCTCAAGTGTGTGCGTATCC  300
        Y  P  D  S  E  S  T  W  E  P  R  Q  N  L  K  C  V  R  I  L

 301  TCAAGCAGTTCCACAAGGACTTAGAAAGGGAGCTGCTCCGGCGGCACCACCGGTCAAAGA  360
        K  Q  F  H  K  D  L  E  R  E  L  L  R  R  H  H  R  S  K  T

 361  CCCCCCGGCACCTGGACCCAAGCTTGGCCAACTACCTGGTGCAGAAGGCCAAGCAGAGGC  420
        P  R  H  L  D  P  S  L  A  N  Y  L  V  Q  K  A  K  Q  R  R

 421  GGGCGCTCCGTCGCTGGGAGCAGGAGCTCAATGCCAAGCGCAGCCATCTGGGACGCATCA  480
        A  L  R  R  W  E  Q  E  L  N  A  K  R  S  H  L  G  R  I  T

 481  CTGTAGAGAATGAGGTGGACCTGGACGGCCCTCCGCGGGCCTTCGTGTACATCAATGAGT  540
        V  E  N  E  V  D  L  D  G  P  P  R  A  F  V  Y  I  N  E  Y

 541  ACCGTGTTGGTGAGGGCATCACCCTCAACCAGGTGGCTGTGGGCTGCGAGTGCCAGGACT  600
        R  V  G  E  G  I  T  L  N  Q  V  A  V  G  C  E  C  Q  D  C

 601  GTCTGTGGGCACCCACTGGAGGCTGCTGCCCGGGGGCGTCACTGCACAAGTTTGCCTACA  660
        L  W  A  P  T  G  G  C  C  P  G  A  S  L  H  K  F  A  Y  N

 661  ATGACCAGGGCCAGGTGCGGCTTCGAGCCGGGCTGCCCATCTACGAGTGCAACTCCCGCT  720
        D  Q  G  Q  V  R  L  R  A  G  L  P  I  Y  E  C  N  S  R  C

 721  GCCGCTGCGGCTATGACTGCCCAAATCGTGTGGTACAGAAGGGTATCCGATATGACCTCT  780
        R  C  G  Y  D  C  P  N  R  V  V  Q  K  G  I  R  Y  D  L  C

 781  GCATCTTCCGGACGGATGATGGGCGTGGCTGGGGCGTCCGCACCCTGGAGAAGATTCGCA  840
        I  F  R  T  D  D  G  R  G  W  G  V  R  T  L  E  K  I  R  K

 841  AGAACAGCTTCGTCATGGAGTACGTGGGAGAGATCATTACCTCAGAGGAGGCAGAGCGGC  900
        N  S  F  V  M  E  Y  V  G  E  I  I  T  S  E  E  A  E  R  R

 901  GGGGCCAGATCTACGACCGTCAGGGCGCCACCTACCTCTTTGACCTGGACTACGTGGAGG  960
        G  Q  I  Y  D  R  Q  G  A  T  Y  L  F  D  L  D  Y  V  E  D

 961  ACGTGTACACCGTGGATGCCGCCTACTATGGCAACATCTCCCACTTTGTCAACCACAGTT 1020
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1021  GTGACCCCAACCTGCAGGTGTACAACGTCTTCATAGACAACCTTGACGAGCGGCTGCCCC 1080
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1081  GCATCGCTTTCTTTGCCACAAGAACCATCCGGGCAGGCGAGGAGCTCACCTTTGATTACA 1140
        I  A  F  F  A  T  R  T  I  R  A  G  E  E  L  T  F  D  Y  N
```

Fig. 7/2

```
1141  ACATGCAAGTGGACCCCGTGGACATGGAGAGCACCCGCATGGACTCCAACTTTGGCCTGG   1200
        M  Q  V  D  P  V  D  M  E  S  T  R  M  D  S  N  F  G  L  A

1201  CTGGGCTCCCTGGCTCCCCTAAGAAGCGGGTCCGTATTGAATGCAAGTGTGGGACTGAGT   1260
        G  L  P  G  S  P  K  K  R  V  R  I  E  C  K  C  G  T  E  S

1261  CCTGCCGCAAATACCTCTTCTAGCCCTTAGAAGTCTGAGGCCAGACTGACTGAGGGGGCC   1320
        C  R  K  Y  L  F  *

1321  TGAAGCTACATGCACCTCCCCCACTGCTGCCCTCCTGTCGAGAATGACTGCCAGGGCCTC   1380

1381  GCCTGCCTCCACCTGCCCCCACCTGCTCCTACCTGCTCTACGTTCAGGGCTGTGGCCGTG   1440

1441  GTGAGGACCGACTCCAGGAGTCCCCTTTCCCTGTCCCAGCCCCATCTGTGGGTTGCACTT   1500

1501  ACAAACCCCCACCCACCTTCAGAAATAGTTTTTCAACATCAAGACTCTCTGTCGTTGGGA   1560

1561  TTCATGGCCTATTAAGGAGGTCCAAGGGGTGAGTCCCAACCCAGCCCCAGAATATATTTG   1620

1621  TTTTTGCACCTGCTTCTGCCTGGAGATTGAGGGGTCTGCTGCAGGCCTCCTCCCTGCTGC   1680

1681  CCCAAAGGTATGGGGAAGCAACCCCAGAGCAGGCAGACATCAGAGGCCAGAGTGCCTAGC   1740

1741  CCGACATGAAGCTGGTTCCCCAACCACAGAAACTTTGTACTAGTGAAAGAAAGGGGTCCC   1800

1801  TGGCCTACGGGCTGAGGCTGGTTTCTGCTCGTGCTTACAGTGCTGGGTAGTGTTGGCCCT   1860

1861  AAGAGCTGTAGGGTCTCTTCTTCAGGGCTGCATATCTGAGAAGTGGATGCCCACATGCCA   1920

1921  CTGGAAGGGAAGTGGGTGTCCATGGGCCACTGAGCAGTGAGAGGAAGGCAGTGCAGAGCT   1980

1981  GGCCAGCCCTGGAGGTAGGCTGGGACCAAGCTCTGCCTTCACAGTGCAGTGAAGGTACCT   2040

2041  AGGGCTCTTGGGAGCTCTGCGGTTGCTAGGGGCCCTGACCTGGGGTGTCATGACCGCTGA   2100

2101  CACCACTCAGAGCTGGAACCAAGATCTAGATAGTCCGTAGATAGCACTTAGGACAAGAAT   2160

2161  GTGCATTGATGGGGTGGTGATGAGGTGCCAGGCACTAGGTAGAGCACCTGGTCCACGTGG   2220

2221  ATTGTCTCAGGGAAGCCTTGAAAACCACGGAGGTGGATGCCAGGAAAGGGCCCATGTGGC   2280

2281  AGAAGGCAAAGTACAGGCCAAGAATTGGGGGTGGGGGAGATGGCTTCCCCACTATGGGAT   2340

2341  GACGAGGCGAGAGGGAAGCCCTTGCTGCCTGCCATTCCCAGACCCCAGCCCTTTGTGCTC   2400

2401  ACCCTGGTTCCACTGGTCTCAAAAGTCACCTGCCTACAAATGTACAAAAGGCGAAGGTTC   2460

2461  TGATGGCTGCCTTGCTCCTTGCTCCCCCACCCCCTGTGAGGACTTCTCTAGGAAGTCCTT   2520

2521  CCTGACTACCTGTGCCCAGAGTGCCCCTACATGAGACTGTATGCCCTGCTATCAGATGCC   2580

2581  AGATCTATGTGTCTGTCTGTGTGTCCATCCCGCCGGCCCCCCAGACTAACCTCCAGGCAT   2640

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Fig. 8

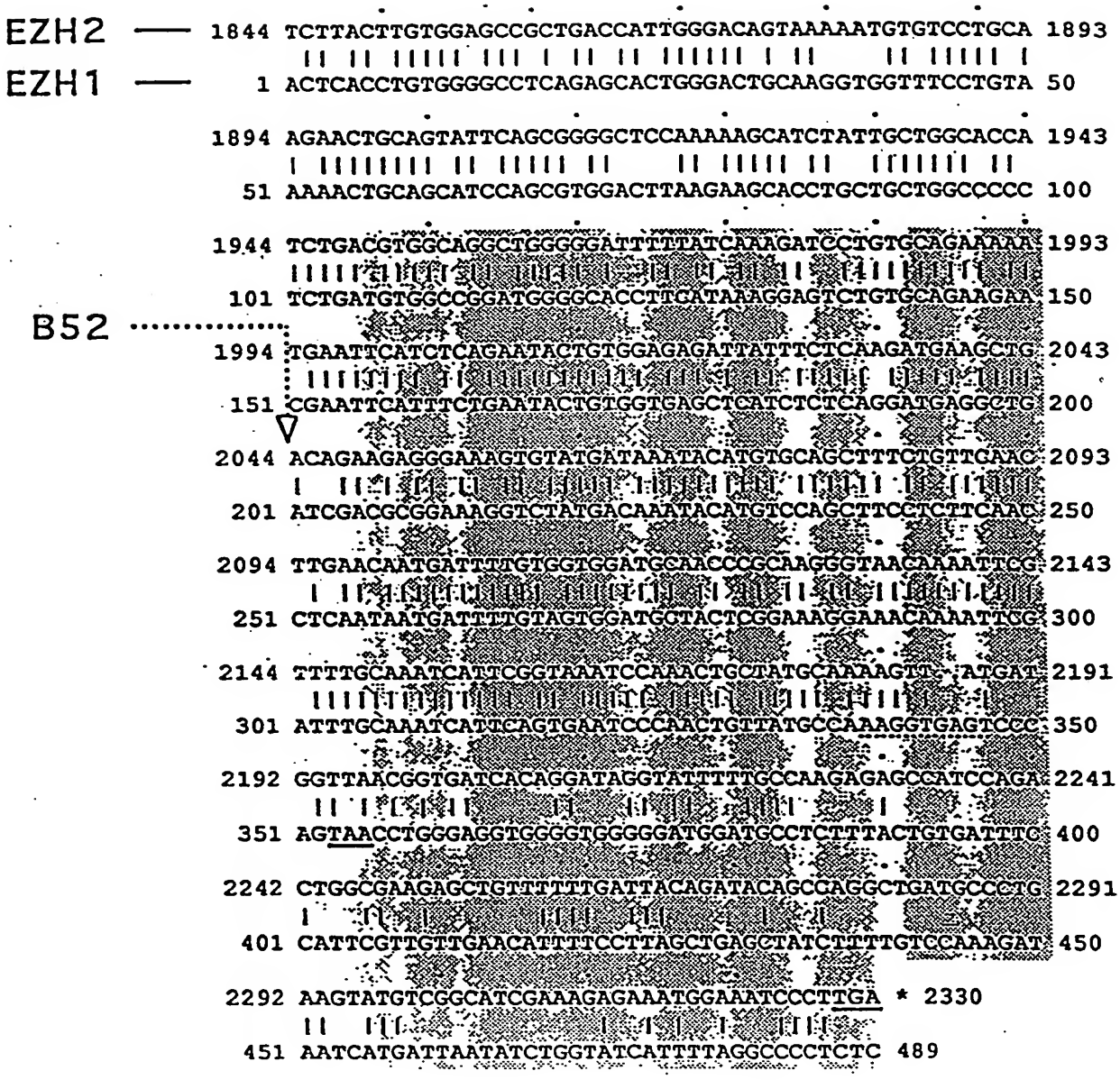

EZH2
EZH1
B52
1844 TCTTACTTGTGGAGCCGCTGACCATTGGGACAGTAAAAATGTGTCCTGCA 1893
1 ACTCACCTGTGGGGCCTCAGAGCACTGGGACTGCAAGGTGGTTTCCTGTA 50
1894 AGAACTGCAGTATTCAGCGGGGCTCCAAAAAGCATCTATTGCTGGCACCA 1943
51 AAAACTGCAGCATCCAGCGTGGACTTAAGAAGCACCTGCTGCTGGCCCCC 100
1944 TCTGACGTGGCAGGCTGGGGGATTTTTATCAAAGATCCTGTGCAGAAAAA 1993
101 TCTGATGTGGCCGGATGGGGCACCTTCATAAAGGAGTCTGTGCAGAAGAA 150
1994 TGAATTCATCTCAGAATACTGTGGAGAGATTATTTCTCAAGATGAAGCTG 2043
151 CGAATTCATTTCTGAATACTGTGGTGAGCTCATCTCTCAGGATGAGGCTG 200
2044 ACAGAAGAGGGAAAGTGTATGATAAATACATGTGCAGCTTTCTGTTCAAC 2093
201 ATCGACGCGGAAAGGTCTATGACAAATACATGTCCAGCTTCCTCTTCAAC 250
2094 TTGAACAATGATTTTGTGGTGGATGCAACCCGCAAGGGTAACAAAATTCG 2143
251 CTCAATAATGATTTTGTAGTGGATGCTACTCGGAAAGGAAACAAAATTCG 300
2144 TTTTGCAAATCATTCGGTAAATCCAAACTGCTATGCAAAAGTT ATGAT 2191
301 ATTTGCAAATCATTCAGTGAATCCCAACTGTTATGCCAAAGGTGAGTCCC 350
2192 GGTTAACGGTGATCACAGGATAGGTATTTTGCCAAGAGAGCCATCCAGA 2241
351 AGTAACCTGGGAGGTGGGGTGGGGGATGGATGCCTCTTTACTGTGATTTC 400
2242 CTGGCGAAGAGCTGTTTTTTGATTACAGATACAGCCAGGCTGATGCCCTG 2291
401 CATTCGTTGTTGAACATTTTCCTTAGCTGAGCTATCTTTTGTCCAAAGAT 450
2292 AAGTATGTCGGCATCGAAAGAGAAATGGAAATCCCTTGA * 2330
451 AATCATGATTAATATCTGGTATCATTTTAGGCCCCTCTC 489

Fig. 9

A

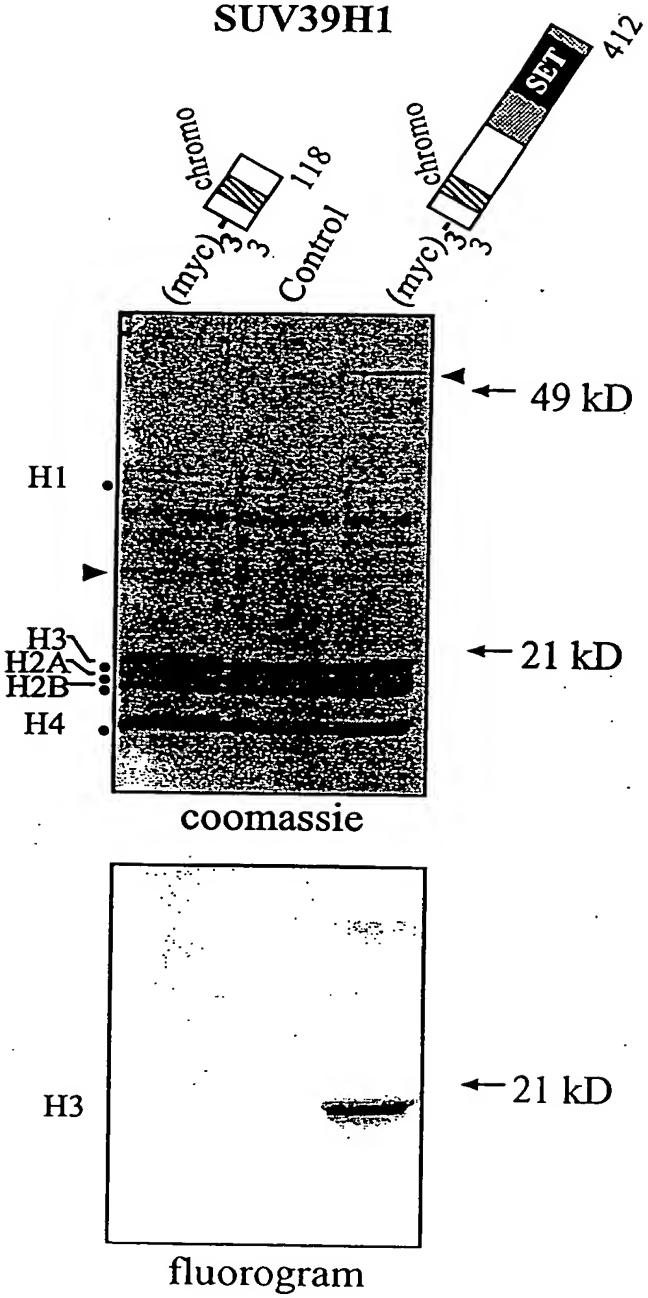

SUV39H1
chromo
SET
412
118
(myc)3
3
Control
49 kD
H1
H3
H2A
H2B
H4
21 kD
coomassie
H3
21 kD
fluorogram

Fig. 9

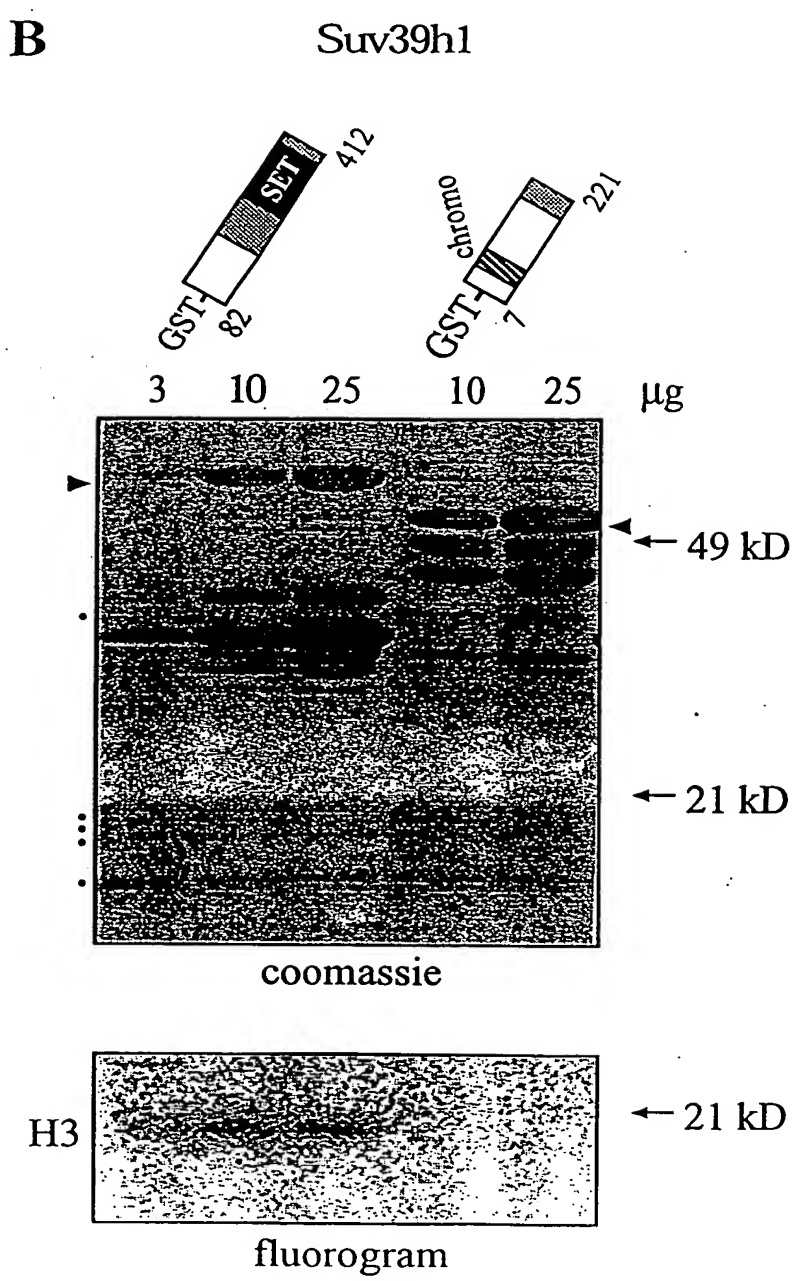

B
Suv39h1
SET
412
GST
82
chromo
221
GST
1
3
10
25
10
25
µg
49 kD
21 kD
coomassie
H3
21 kD
fluorogram

Fig. 10

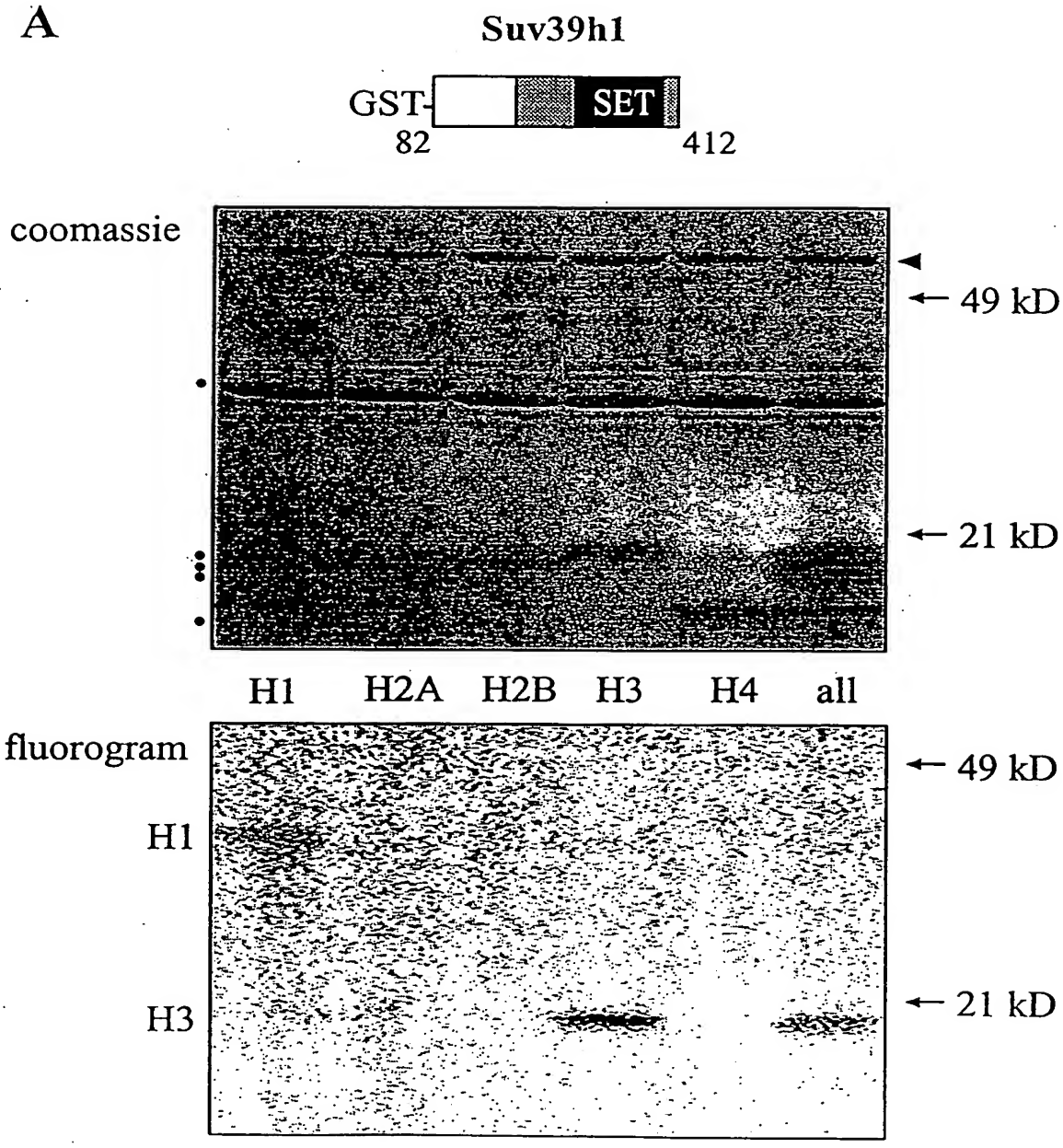
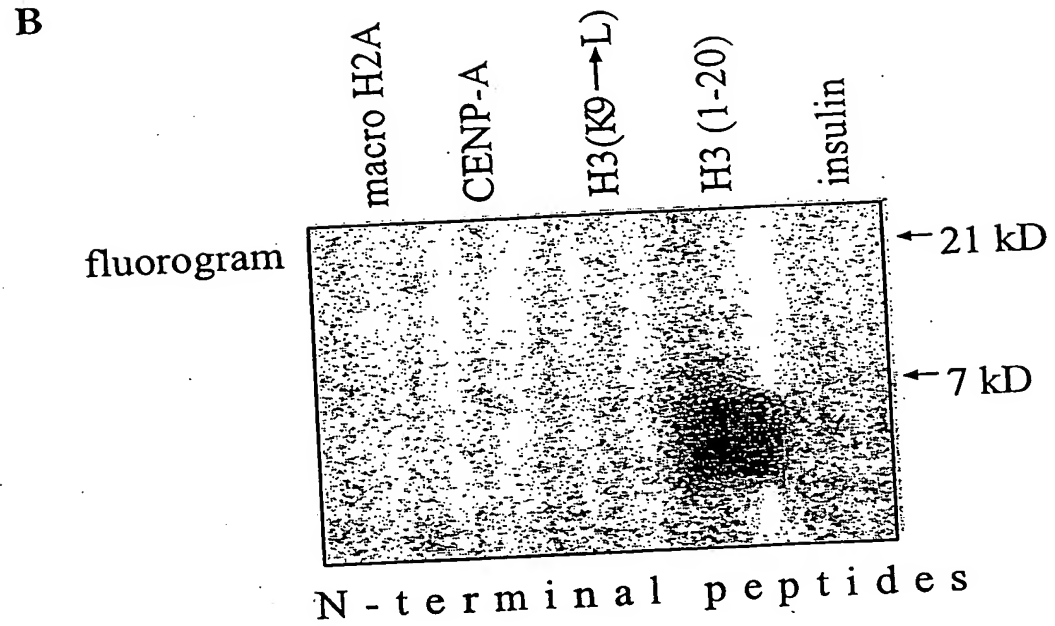
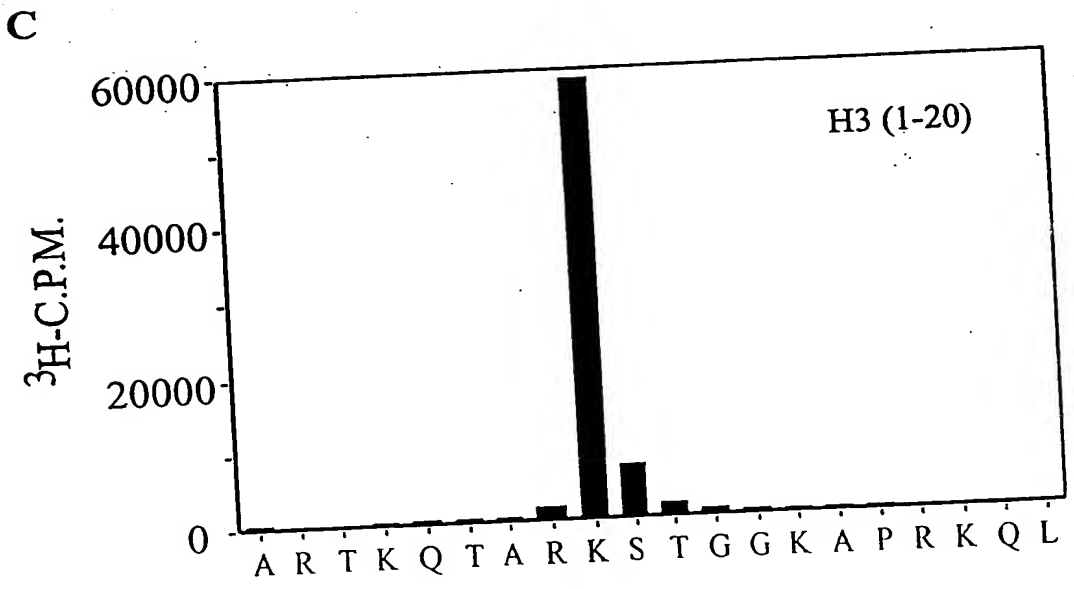

A
Suv39h1
GST-
SET
82
412
coomassie
49 kD
21 kD
H1
H2A
H2B
H3
H4
all
fluorogram
H1
H3
49 kD
21 kD

Fig. 10


B
macro H2A
CENP-A
H3(K9→L)
H3 (1-20)
insulin
fluorogram
21 kD
7 kD
N-terminal peptides


C
60000
40000
20000
0
^{3}H-C.P.M.
H3 (1-20)
A R T K Q T A R K S T G G K A P R K Q L